WHAT IS CLAIMED IS:

1. A trehalose synthase protein with the following amino acid sequence:

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Met Ser Ile Pro Asp Asn Thr Tyr Ile Glu Trp Leu Val Ser Gln
              5                 10                  15
Ser Met Leu His Ala Ala Arg Glu Arg Ser Arg His Tyr Ala Gly
             20                 25                  30
Gln Ala Arg Leu Trp Gln Arg Pro Try Ala Gln Ala Arg Pro Arg
             35                 40                  45
Asp Ala Ser Ala Ile Ala Ser Val Trp Phe Thr Ala Tyr Pro Ala
             50                 55                  60
Ala Ile Ile Thr Pro Glu Gly Gly Thr Val Leu Glu Ala Leu Gly
             65                 70                  75
Asp Asp Arg Leu Trp Ser Ala Leu Ser Glu Leu Gly Val Gln Gly
             80                 85                  90
Ile His Asn Gly Pro Met Lys Arg Ser Gly Gly Leu Arg Gly Arg
             95                100                 105
Glu Phe Thr Pro Thr Ile Asp Gly Asn Phe Asp Arg Ile Ser Phe
            110                115                 120
Asp Ile Asp Pro Ser Leu Gly Thr Glu Glu Gln Met Leu Gln Leu
            125                130                 135
Ser Arg Val Ala Ala Ala His Asn Ala Ile Val Ile Asp Asp Ile
            140                145                 150
Val Pro Ala His Thr Gly Lys Gly Ala Asp Phe Arg Leu Ala Glu
            155                160                 165
Met Ala Tyr Gly Asp Tyr Pro Gly Leu Tyr His Met Val Glu Ile
            170                175                 180
Arg Glu Glu Asp Trp Glu Leu Leu Pro Glu Val Pro Ala Gly Arg
            185                190                 195
Asp Ser Val Asn Leu Leu Pro Pro Val Val Asp Arg Leu Lys Glu
            200                205                 210
Lys His Tyr Ile Val Gly Gln Leu Gln Arg Val Ile Phe Phe Glu
            215                220                 225
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         Pro Gly Ile Lys Asp Thr Asp Trp Ser Val Thr Gly Glu Val Thr
                          230                 235                 240
         Gly Val Asp Gly Lys Val Arg Arg Trp Val Tyr Leu His Tyr Phe
                          245                 250                 255
         Lys Glu Gly Gln Pro Ser Leu Asn Trp Leu Asp Pro Thr Phe Ala
                          260                 265                 270
         Ala Gln Gln Leu Ile Ile Gly Asp Ala Leu His Ala Ile Asp Val
                          275                 280                 285
         Thr Gly Ala Arg Val Leu Arg Leu Asp Ala Asn Gly Phe Leu Gly
                          290                 295                 300
         Val Glu Arg Arg Ala Glu Gly Thr Ala Trp Ser Glu Gly His Pro
                          305                 310                 315
         Leu Ser Val Thr Gly Asn Gln Leu Leu Ala Gly Ala Ile Arg Lys
                          320                 325                 330
         Ala Gly Gly Phe Ser Phe Gln Glu Leu Asn Leu Thr Ile Asp Asp
                          335                 340                 345
         Ile Ala Ala Met Ser His Gly Gly Ala Asp Leu Ser Tyr Asp Phe
                          350                 355                 360
         Ile Thr Arg Pro Ala Tyr His His Ala Leu Leu Thr Gly Asp Thr
                          365                 370                 375
         Glu Phe Leu Arg Met Met Leu Arg Glu Val His Ala Phe Gly Ile
                          380                 385                 390
         Asp Pro Ala Ser Leu Ile His Ala Leu Gln Asn His Asp Glu Leu
                          395                 400                 405
         Thr Leu Glu Leu Val His Phe Trp Thr Leu His Ala Tyr Asp His
                          410                 415                 420
         Tyr His Tyr Lys Gly Gln Thr Leu Pro Gly Gly His Leu Arg Glu
                          425                 430                 435
         His Ile Arg Glu Glu Met Tyr Glu Arg Leu Thr Gly Glu His Ala
                          440                 445                 450
         Pro Tyr Asn Leu Lys Phe Val Thr Asn Gly Val Ser Cys Thr Thr
                          455                 460                 465
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Ala Ser Val Ile Ala Ala Ala Leu Asn Ile Arg Asp Leu Asp Ala
            470             475             480
Ile Gly Pro Ala Glu Val Glu Gln Ile Gln Arg Leu His Ile Leu
            485             490             495
Leu Val Met Phe Asn Ala Met Gln Pro Gly Val Phe Ala Leu Ser
            500             505             510
Gly Trp Asp Leu Val Gly Ala Leu Pro Leu Ala Pro Glu Gln Val
            515             520             525
Glu His Leu Met Gly Asp Gly Asp Thr Arg Trp Ile Asn Arg Gly
            530             535             540
Gly Tyr Asp Leu Ala Asp Leu Ala Pro Glu Ala Ser Val Ser Ala
            545             550             555
Glu Gly Leu Pro Lys Ala Arg Ser Leu Tyr Gly Ser Leu Ala Glu
            560             565             570
Gln Leu Gln Arg Pro Gly Ser Phe Ala Cys Gln Leu Lys Arg Ile
            575             580             585
Leu Ser Val Arg Gln Ala Tyr Asp Ile Ala Ala Ser Lys Gln Ile
            590             595             600
Leu Ile Pro Asp Val Gln Ala Pro Gly Leu Leu Val Met Val His
            605             610             615
Glu Leu Pro Ala Gly Lys Gly Val Gln Leu Thr Ala Leu Asn Phe
            620             625             630
Ser Ala Glu Pro Val Ser Glu Thr Ile Cys Leu Pro Gly Val Ala
            635             640             645
Pro Gly Pro Val Val Asp Ile Ile His Glu Ser Val Glu Gly Asp
            650             655             660
Leu Thr Asp Asn Cys Glu Leu Gln Ile Asn Leu Asp Pro Tyr Glu
            665             670             675
Gly Leu Ala Leu Arg Val Val Ser Ala Ala Pro Pro Val Ile
            680             685
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2. A trehalose synthase gene with the following nucleotide sequence:

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GATCGCTGGC GTACTGCAGG TAGAGCAGGC GCATCGGCCC CCAGGGCGCA TCGGCCGGCT      60
CCGCTGTGCC CTGCTGGTTC ATGAAGCGGA CGAAGCGGCC ATCGCGGAAC CGTGGACGCC      120
ATTCGGGGCT GTCCGGGTCG CGGCTGTCGG TGAGCGTGCG CCACAGGTCG CTGCGAAACG      180
GCGGACCGCT CCAAAGCGCG CCGTGGATGG GATCGCCGAG CAGTTCGTGC AGCTCCCAGG      240
AACGTTGCGA ATGCAGCGCG CCGAGGCTCA GGCCATGCAG ATACAGGCGC GGTCGGCGTT      300
CGGCCGGCAG TTCGGTCCAG TAGCCATAGA TCTCGGCGAA TAGCGCGCGG CCACGTCGC      360
GGCCGTAGTC GGCCTCCACC AGCAGCGCCA GCGGGCTGTT CAGATAGGAG TACTGCAACG      420
CCACGCTGGC GATATCGCCG TGGTGCAGGT ATTCCACTGC GTTCATCGCC GCCGGGTCGA      480
TCCAGCCGGT ACCGGTGGGC GTCACCAGCA CCAGCACCGA TCGCTCGAAG GCGCCGCTGC      540
GCTGCAGCTC GCGCAAGGCC AGACGCGCCC GCTGGCGCGG GGTCTCTGCC GCGCGCAGAC      600
CGACGTAGAC GCGAATCGGC TCGAGCGCCG AGCGGCCGCT CAAGACGCTG ATATCCGCCG      660
CCGACGGGCC GGAGCCGATG AACTCGCGGC CGGTGCGGCC CAGCTCCTCC CAGCGCAGCA      720
ACGAGGCCCG GCTGCCGCTT TTCAGCGGCG AGGCCGGTGG CGCCGTCTCC GGTTCGATCA      780
GGGCGTCGTA CTGCGCGAAG GATGCGTCCA GCATGCGCAG TGCCCGCGCC GCCAGCACAT      840
CGCTGAGCAG CGACCAGAAC AGCGCCAGCG CCACCAGCAC GCCGATCACG TTGGCCAGGC      900
GCCGTGGCAG CACGCGGTCG GCGTGCCGCG AGACGAAGCG CGACACCAGC CGATACAGAC      960
GCGCCAGCGT CAGCAGGATG AGAAAGGTCG CCAGCGCGGT GAGAATGACT TCGAGCAGGT     1020
GCGCACTGCT CACCGGCGGC ATGCCCATCA GCGCGCGTAC CGCGTTCTGC CAGCCGGCGA     1080
CCTGGCTGAG GAAATACCCG GCCAGCAGCA GGCAGCCGAC CGCGATCAGC AGATTGACCC     1140
GCTCGCGCTG CCAGCCTGGG CGCTCCGGCA GTTCCAGATA GCGCCACAGC CAGCGCCAGA     1200
ACACGCCGAG GCCATAGCCC ACCGCCAGCG CCGCGCCGGC CAGCACGCCC TGGCTCAGCG     1260
TCGAGCGCGG CAGCAGCGAT GGCGTCAGCG CCGCGCAGAA GAACAGCGTG CCCAGCAGCA     1320
GGCCGAAACC GGACAGCGAG CGCCAGATAT AGAGGACGGG CAGGTGCAGC ATGAAGATCT     1380
CCGCGGTCGG GTGACGGCGT CGCGCCTCGG CATATCGAGG CGTGTCCGGT CGTGCGGTTC     1440
CCGTGATGGT CCGCAGCAGG CCAATCCGAT GCAACGATGG CCGAGCGGCC GACTCAAACG     1500
TCTACATTTC CCTAGTGCTG CCGGAACCGA TCGCCG                               1536
ATG AGC ATC CCA GAC AAC ACC TAT ATC GAA TGG CTG GTC AGC CAG TCC     1584
ATG CTG CAT GCG GCC CGC GAG CGG TCG CGT CAT TAC GCC GGC CAG GCG     1632
CGT CTC TGG CAG CGG CCT TAT GCC CAG GCC CGC CCG CGC GAT GCC AGC     1680
GCC ATC GCC TCG GTG TGG TTC ACC GCC TAT CCG GCG GCC ATC ATC ACG     1728
CCG GAA GGC GGC ACG GTA CTC GAG GCC CTC GGC GAC GAC CGC CTC TGG     1776
AGT GCG CTC TCC GAA CTC GGC GTG CAG GGC ATC CAC AAC GGG CCG ATG     1824
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AAG CGT TCC GGT GGC CTG CGC GGA CGC GAG TTC ACC CCG ACC ATC GAC        1872
GGC AAC TTC GAC CGC ATC AGC TTC GAT ATC GAC CCG AGC CTG GGG ACC        1920
GAG GAG CAG ATG CTG CAG CTC AGC CGG GTG GCC GCG GCG CAC AAC GCC        1968
ATC GTC ATC GAC GAC ATC GTG CCG GCA CAC ACC GGC AAG GGT GCC GAC        2016
TTC CGC CTC GCG GAA ATG GCC TAT GGC GAC TAC CCC GGG CTG TAC CAC        2064
ATG GTG GAA ATC CGC GAG GAG GAC TGG GAG CTG CTG CCC GAG GTG CCG        2112
GCC GGG CGT GAT TCG GTC AAC CTG CTG CCG CCG GTG GTC GAC CGG CTC        2160
AAG GAA AAG CAC TAC ATC GTC GGC CAG CTG CAG CGG GTG ATC TTC TTC        2208
GAG CCG GGC ATC AAG GAC ACC GAC TGG AGC GTC ACC GGC GAG GTC ACC        2256
GGG GTC GAC GGC AAG GTG CGT CGC TGG GTC TAT CTG CAC TAC TTC AAG        2304
GAG GGC CAG CCG TCG CTG AAC TGG CTC GAC CCG ACC TTC GCC GCG CAG        2352
CAG CTG ATC ATC GGC GAT GCG CTG CAC GCC ATC GAC GTC ACC GGC GCC        2400
CGG GTG CTG CGC CTG GAC GCC AAC GGC TTC CTC GGC GTG GAA CGG CGC        2448
GCC GAG GGC ACG GCC TGG TCG GAG GGC CAC CCG CTG TCC GTC ACC GGC        2496
AAC CAG CTG CTC GCC GGG GCG ATC CGC AAG GCC GGC GGC TTC AGC TTC        2544
CAG GAG CTG AAC CTG ACC ATC GAT GAC ATC GCC GCC ATG TCC CAC GGC        2592
GGG GCC GAT CTG TCC TAC GAC TTC ATC ACC CGC CCG GCC TAT CAC CAT        2640
GCG TTG CTC ACC GGC GAT ACC GAA TTC CTG CGC ATG ATG CTG CGC GAA        2688
GTG CAC GCC TTC GGC ATC GAC CCG GCG TCA CTG ATC CAT GCG CTG CAG        2736
AAC CAT GAC GAG TTG ACC CTG GAG CTG GTG CAC TTC TGG ACG CTG CAC        2784
GCC TAC GAC CAT TAC CAC TAC AAG GGC CAG ACC CTG CCC GGC GGC CAC        2832
CTG CGC GAA CAT ATC CGC GAG GAA ATG TAC GAG CGG CTG ACC GGC GAA  __    2880
CAC GCG CCG TAC AAC CTC AAG TTC GTC ACC AAC GGG GTG TCC TGC ACC        2928
ACC GCC AGC GTG ATC GCC GCG GCG CTT AAC ATC CGT GAT CTG GAC GCC        2976
ATC GGC CCG GCC GAG GTG GAG CAG ATC CAG CGT CTG CAT ATC CTG CTG        3024
GTG ATG TTC AAT GCC ATG CAG CCC GGC GTG TTC GCC CTC TCC GGC TGG        3072
GAT CTG GTC GGC GCC CTG CCG CTG GCG CCC GAG CAG GTC GAG CAC CTG        3120
ATG GGC GAT GGC GAT ACC CGC TGG ATC AAT CGC GGC GGC TAT GAC CTC        3168
GCC GAT CTG GCG CCG GAG GCG TCG GTC TCC GCC GAA GGC CTG CCC AAG        3216
GCC CGC TCG CTG TAC GGC AGC CTG GCC GAG CAG CTG CAG CGG CCA GGC        3264
TCC TTC GCC TGC CAG CTC AAG CGC ATC CTC AGC GTG CGC CAG GCC TAC        3312
GAC ATC GCT GCC AGC AAG CAG ATC CTG ATT CCG GAT GTG CAG GCG CCG        3360
GGA CTC CTG GTG ATG GTC CAC GAG CTG CCT GCC GGC AAG GGC GTG CAG        3408
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CTC ACG GCA CTG AAC TTC AGC GCC GAG CCG GTC AGC GAG ACC ATC TGC        3456
CTG CCC GGC GTG GCG CCC GGC CCG GTG GTG GAC ATC ATT CAC GAG AGT        3504
GTG GAG GGC GAC CTC ACC GAC AAC TGC GAG CTG CAG ATC AAC CTC GAC        3552
CCG TAC GAG GGG CTT GCC CTG CGT GTG GTG AGC GCC GCG CCG CCG GTG        3600
ATC TGA GCGC                                                           3610
CCTCTTCGCG CGCCCCGGGT CCGCCGCTAT AGTGCGCAGC GCCTGGGGCG CGCATTGCCC      3670
TCGCCGTCGA GACCAGCCCG TGTCGTTCAC TTCGCTTTTC CGCCTTGCGC TGCTGCCGCT      3730
GGCGCTGCTT GCCGCACCCG TCTGGGCGCA GACCGCCTGC CCGCCCGGCC AGCAGCCGAT      3790
CTGCCTGAGC GGCAGCTGCC TCTGCGTGCC GGCCGCCGCC AGCGATCCAC AGGCGGTCTA      3850
CGACCGCGTG CAGCGTATGG CTACGCTGGC CCTGCAGAAC TGGATCCAGC AGTCGCGCGA      3910
CCGCCTGATG GCCGGCGGCG TCGAGCCGAT ACCGCTGCAC ATCCGCTCGC AGCTCGAGCC      3970
GTATTTCGAT CTTGCCGTGC TGGAGAGTGC GCGGTACCGC GTCGGCGACG AGGTGGTGCT      4030
GACTGCCGGC AACACCCTGC TGCGCAACCC GGACGTCAAT GCCGTGACCC TGATCGACGT      4090
CATCGTCTTC CGCCACGAGG AGGATGCCCG GGACAACGTC GCGCTCTGGG CCCATGAGCT      4150
CAAGCACGTC GAGCAATATC TGGACTGGGG CGTCGCCGAG TTCGCCCGGC GCTATACGCA      4210
GGATTTCCGT GCCGTGGAGC GCCCGGCCTA TGCGCTGGAG CGTGAGGTGG AAGAGGCCCT      4270
GCGCGAGACG CAGACGCGGC GCTGAGCGAG CTGATCGGTG CTGCTGCCCG CACTGGGCTG      4330
AAGCCCACCA ATGACGCCGG CGAAAACGAA AAACCCCGCC GAGGCGGGGT TTCTGACGCG      4390
GGTTGTGCGG TCAGCTCAGA ACGCCGGGAC CACGGCGCCC TTGTACTTTT CCTCGATGAA      4450
CTGGCGTACT TGCTCGCTGT GCAGCGCGGC AGCCAGTTTC TGCATGGCAT CGCTGTCCTT      4510
GTTGTCCGGA CGGGCGACCA GAATGTTCAC GTATGGCGAG TCGCTGCCCT CGATCACCAG      4570
GGCGTCCTGG GTCGGGTTCA GCTTGGCTTC CAGCGCGTAG TTGGTGTTGA TCAGCGCCAG      4630
GTCGACCTGG GTCAGCACGC GCGGCAGAGT CGCGGCTTCC AGTTCGCGGA TCTTGATCTT      4690
CTTCGGGTTC TCGGCGATGT CTTCGGCGTG GCGGTGATGC CGGCGCCGTC CTTCAGACCG      4750
ATC                                                                   4753
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3. A recombinant plasmid containing the trehalose synthase gene of claim 1.

4. The recombinant plasmid according to claim 1 which is recombinant plasmid pCJ122.

5. A transformed E. coli with the recombinant plasmid of claim 1.

6. The transformant according to claim 5 in which the recombinant plasmid is pCJ122.

7. A process for producing trehalose which comprises reacting the trehalose synthase enzyme of claim 1 with maltose solution to obtain trehalose.

8. A process for producing trehalose which comprises crushing the transformed E. coli of claim 5, centrifuging the crushed bacteria, and reacting the resulting supernatant with maltose solution to obtain trehalose.

9. A novel microorganism *Pseudomonas stutzeri* CJ38 that produces trehalose from maltose.

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